

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 11:29:22 ; Search time 4179.27 Seconds
(wtihout alignments)
6378.264 Million cell updates/sec

Title: US-09-052-089A-8
Perfect score: 1975
Sequence: GGCAGAGGGGCGGAGC.....CAA.....AAAAAAA 1975
scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: em_estba: *
2: em_esthun: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1896	96.0	2696	AK012948
2	1886.2	95.5	1938	AK012948
3	671.2	34.0	887	AK012948
4	669.2	33.9	959	AL560912
5	641.2	32.5	702	BI151643
6	634.2	32.1	687	BF658170
7	632.6	32.0	744	BF162255
8	603.0	30.5	10	BM46844
9	568.2	28.8	608	BI69519
10	539.3	27.3	589	BE334637
11	532.9	26.9	554	AA684194
12	514.4	26.0	702	BG764118
13	513.6	26.0	752	BG682548
14	513.4	26.0	519	BE304189
15	510.6	25.9	784	BG120736
16	504.2	25.5	908	BG420765
17	503.2	25.5	825	BE546559

RESULTS

RESULT	1
ACCESSION	AK012948
DEFINITION	Mus musculus 10, 11 days embryo whole body mRNA linear HTC 19-JAN-2002 enriched library clone:2810054N23:TRAF-1-interacting protein, full insert sequence.
VERSION	AK012948.1
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) 10, 11 days embryo mRNA, clone lib:RIKEN full-length enriched mouse cDNA library clone:2810054N23.
ORGANISM	Mus musculus
REFERENCE	Carninci,P., Mammalia; Butcheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Carninci,P. and Hayashizaki,Y. (1999) High efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
JOURNAL	
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2 (sites)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugihara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3 (sites)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawaji,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1577-1771 (2000)

ALIGNMENTS

RESULT	1
ACCESSION	AK012948
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KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) 10, 11 days embryo mRNA, clone lib:RIKEN full-length enriched mouse cDNA library clone:2810054N23.
ORGANISM	Mus musculus
REFERENCE	Carninci,P., Mammalia; Butcheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Carninci,P. and Hayashizaki,Y. (1999) High efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
JOURNAL	
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2 (sites)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugihara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3 (sites)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawaji,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1577-1771 (2000)

Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues. First strand cDNA was primed with a primer
 [5'-GAGGAGAGAGGAGATCCAGCTTGTGTTGTTGTTGTT-3']. cDNA was
 prepared by using Trehalose reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went
 through one round of normalization to ROT = 7.5 and subtraction to
 ROT = 37.5. Second strand cDNA was prepared with the primer adapter
 of sequence [5'-CGAGGAGGACCTCGAGTTAAATTAAATTCATCCCCCCCCC 3']. cDNA was cleaved
 with XbaI and SstI. Cloning sites, 5' end: XbaI; 3' end: SstI.
 Host: SOLR.

source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGI:MGI-1898099"
/clone="2810021M05"
/dev_stage="10, 11 days embryo"
95 .1507
/gene="Trailp"
95 .1507
/gene="Trailp"
/note="TRAF-interacting protein
data source:MGI, source key:MGI:1096377, evidence::ISS
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/db_xref="GI-12849759"
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TCPQCRTQVKKTTIKFLFLQAEENWDLAFTLKEFLDSYKAQSLQDRERKDSQA
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CXKTMEOELLIQSOSRVEEENIDMKGQSVASEQVYCUSIKKTEENLKEKAT
GELADRLKKDKVASSRSKQSRTEKLNFEDLSRQADQETLSRQADQETLSRQADQET
TLSUPPAMENTVSRLVESPAPVEMMPRLHOPPFGEIDLNTFDNTTPQTSQ
RCLPRKGGLERAKSPMQNWLKKHKVSKPEQLSLLGGORCVGLDEELAGAPLFIRN
AVLGQKOPNRRTAESRECSDTDVRIIGFQDGGRRTKFQPRDTTIRPVPKSKASKOK
VRIKTVSSASQPUDTFEQ"
BASE COUNT
 506 a 486 c 527 g 419 t
ORIGIN
Query Match 95.5%; Score 1886.2; DB 11; Length 1938;
Best Local Similarity 99.3%; Pred. NO: 0;
Matches 1926; Conservative 0; Mismatches 8; Indels 5; Gaps 3;
QY 21 GAAMTTGAGGAACCGGAGGCCGGGGCGGT --CCACCAAATGTGCTCTGCTCGC 77
Db 1 GARAAATTGAGGAACCGGAGGCCGGGGCGGTCTGGCCACCAACTGTGCTCTGCTCGC 60
QY 78 AGCTGGTGCCTGGCTGTGACTGACCATGCTATCTCTCTCTGTGCACTAT 137
Db 61 AGCGGGTTCTGGGCTGTGACTGACCATGCTATCGCGCTCTGGCACAT 120
QY 138 CTGCTCCGACTCTTCGATACCTCCCGTGACGCGTGGCTCCATCACTGTGCACTAT 197
Db 121 CTGCTCCGACTCTTCGATACCTCCCGTGACGCGTGGCTCCATCACTGTGCACTAT 180
QY 198 TCATCTGGCATGCTTAATCCAGCTGTTGAGACAGCACCAGCTGGACCTGCCAACAGT 257
Db 181 TCATCTGGCATGCTTAATCCAGCTGTTGAGACAGCACCAGCTGGACCTGCCAACAGT 240
QY 258 TAGATCCAGGTGGCAAAAGACTATATAACAACATTTCTGTGACCTGCCAACAGT 317
Db 241 TAGATCCAGGTGGCAAAAGACTATATAACAACATTTCTGTGACCTGCCAACAGT 300
QY 318 AGAGGAGATGCTGTTGAGACGATTCATAAGAATGACAGCAGCTGCAAGACCA 377
Db 301 AGAGGAGATGCTGTTGAGACGATTCATAAGAATGACAGCAGCTGCAAGACCA 360
QY 541 CAAACAGCTGGAGGCCACGGCTCAAGCTGAGATGAAAGATGGCAAT 600
Db 601 TGACTCTRACTCCAGAGCCAGCTTCTAGGGAGGATGTTGAGACATGGGT 677
QY 678 GGGACAGTCAAGGGAGGAGCTGGCTGTGACTGCGTGTGCTCCAGAAAGATGTA 737
Db 661 GGGACAGTCAGCGGTGAGCAGCTGGCTGTGACTGCGTGTGCTCCAGAAAGATGTA 720
QY 738 GAACCTGAAGAACCTGGCAAGCTGAGACTCTCACACACTGAGCTGATAGGGCAAGTGA 797
Db 721 GAATCTGAAGGAAGCTGGAGGCCACAGGGAACTGGTGAAGAGGATTT 780
QY 798 GGTGTCCTCTAGGACCAAGTGTGAGACTCTCACACACTGAGCTGATAGGGCAAGTGA 857
Db 781 GGTCCTCTAGGACCAAGTGTGAGACTCTCACACACTGAGCTGATAGGGCAAGTGA 840
QY 858 ACTGAGGTGAGCCAGAAGGACTACAAAGTGTGACCCAGGAGATCAGGCTTAAGAA 917
Db 841 ACTGAGGTGAGCCAGAAGGACTACAAAGTGTGACCCAGGAGATCAGGCTTAAGAA 900
QY 918 GAAGCTGTATGATCTCTCCAGGACCTCTGAGCCATGCTCC -GGACGATATGAGACGTC 976
Db 901 GAAG -CTGATGATCCTCTAGGACCTCTGAGCCATGCTCCGGGACGATAGCAGTC 959
QY 977 GCCCTCTGTTTGAGACCCACCCCTGTGGAGATGATGAAACCCAGGGCTCACCGC 1036
Db 960 GCGCCCTGCTTGGAGACCCACCCCTGTGGAGATGATGAAACCCAGGGCTCACCGC 1019
QY 1037 CACCTCTGGTATGAGATTGATCTCAAATACCACTTGATGTAATAACCCCTCCAAACC 1096
Db 1020 CACCTCTGGTATGAGATTGATCTCAAATACCACTTGATGTAATAACCCCTCCAAACC 1079
QY 1097 AGACCTCTGGTCTCCAGCATGCTCCCAAGAAGCTGCTGCTGGTGAAGGGCACGCTC 1156
Db 1080 AGACCTCTGGTCTCCAGCATGCTCCCAAGAAGCTGCTGCTGGTGAAGGGCACGCTC 1139
QY 1157 CCATGAGATGCTCTAGAAGGTGCAAAAGTCTCCAGGGGAAATCCAGCTC 1216
Db 1140 CCATGAGATGCTCTAGAAGGTGCAAAAGTCTCCAGGGGAAATCCAGCTC 1199
QY 1217 TGGGTGGCCAGCGATGTGAGGAGCTAGATGAGGAACTGGCTGGAGCCTCCCTCT 1276
Db 1200 TGGGTGGCCAGCGATGTGAGGAGCTAGATGAGGAACTGGCTGGAGCCTCCCTCT 1259
QY 1277 TCATCCGATATGCTGTCAGGACACAGGCCACAGGACCAAGCTGCAAAACTCTCA 1336
Db 1260 TCATCCGATATGCTGTCAGGACACAGGCCACAGGACCAAGCTGCAAAACTCTCA 1319
QY 1337 GCAGCACAGATGTGAGATGAGCTTGTAGGGCTGTGGAGACGACAAATTCATCC 1396
Db 1320 GCACACAGATGTGAGATGAGCTTGTAGGGCTGTGGAGACGACAAATTCATCC 1379
QY 1397 AGCTGAGCACACACATATCCGACCAAGTGGCTGTGAGTCCAAGCCAAAGTAAAC 1456
Db 1380 AGCTAGGGACACACCATATCCGACCAAGTGGCTGTGAGTCCAAGCCAAAGTAAAC 1439
QY 1457 AGAAAGTGAAGAATGAGACTGCTGAGTGTGCTCCGCCAGCTGATACCTCTCT 1516

http://fulllength.invitrogen.com"						
	LOCUS	BASE COUNT	EST	LINEAR	ORIGIN	
Qy	1440 AGRAAGTGGAAATAAAGACTGTGTCATGCCCTCCACCCAAAGCTGGATACTCTTAT	1499				
Qy	1517 GTCAGTGAACTGGGACCGCAGAGTAGTTGCAATTAGGGCCAGAACCTGCCAACCG	1576				
Db	1500 GTGAGTGACGGGAGGACAGAGTAGTGTGCAATTAGGGCCAGAACCTGCCAACCG	1559				
Qy	1577 AAGTGTGTTGGAGATGCTCTTGACCAAGAGATGTCAGAGAGATGCCAGAACACA	1636				
Db	1560 AAGTGTGTTGGAGATGCTCTTGACCAAGAGATGTCAGAGAGATGCCAGAACACA	1619				
Qy	1637 CTTCCTGTTCTACTGCGCCCTCACCACTGGAACACTGACAGTACTGTC	1696				
Db	1620 CTTCCTGTTCTACTGCGCCCTCACCACTGGAACACTGACAGTACTGTC	1679				
Qy	1697 CGATCAGAGGAGGCTACTCCAGTTGAGGGTTTGCTTATACCTACACCAAGTCGCG	1756				
Db	1680 CGATCAGAGGAGGCTACTCCAGTTGAGGGTTTGCTTATACCTACACCAAGTCGCG	1739				
Qy	1757 TGGACTCTTGTATAGACAGGCTCACATTGACTCTAGTGGATGGAGTGCTG	1816				
Db	1740 TGGACTCTTGTATAGACAGGCTCACATTGACTCTAGTGGATGGAGTGCTG	1799				
Qy	1817 GAGATCCATGAGGCTGAGGACCCGGCTGAGA 1859	1876				
Db	1800 GAGATCCATGAGGCTGAGGACCCGGCTGAGA 1859	1859				
Qy	1877 GCTGAAATTATGGGTAGGGTGTAGTGGAAAGGTGGGAAAGTTCTGTGAAA	1936				
Db	1860 GCTGAAATTATGGGTAGGGTGTAGTGGAAAGGTGGGAAAGTTCTGTGAAA	1919				
Qy	1937 TAAAGGGATCTTCTT 1955					
Db	1920 TAAAAGGCATCTTCTT 1938					
RESULT	3					
AL560912						
LOCUS	AL560912	887	bp	mRNA	linear	EST 16-FEB-2001
DEFINITION	AL560912 LTR_NFL010_B2C	Homo sapiens	cDNA	clone	CS0DL005YI08	5
PRIMER	mRNA sequence.					
ACCESSION	AL560912					
VERSION	AL560912.1					
KEYWORDS	EST.					
COMMENT	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished (2001)					
CONTACT	Contact: Genoscope					
GENOSCOPE	Genoscope - Centre National de Séquençage					
BP	191 91006 EVRY cedex - France					
Email:	seqgen@genoscope.cns.fr , Web : www.genoscope.cns.fr .					
FEATURES	source					
/organism="Homo sapiens"						
/clone="cS0D005YI08"						
/clone_lib="LTL_NFL010_B2C"						
/sex="male"						
/tissue_type="B cells from Burkitt lymphoma"						
/note="vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliangell@tech.com URL : http://fulllength.invitrogen.com"						
RESULT	4					
AL560947						
LOCUS	AL560947	959	bp	mRNA	linear	EST 16-FEB-2001

		REFERENCE
BASE COUNT	ORIGIN	AUTHORS
186 a	Query Match	1 (bases 1 to 687)
182 c	Best Local Similarity	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
190 g	Library constructed by Life Technologies. Investigator	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
144 t	Providing samples: Gilbert Smith, NIH*	Tumor Gene Index
		Unpublished (1997)
		Contact: Robert Strausberg, Ph.D.
		Email: cgaps-r@mail.nih.gov
		This clone is available royalty-free through LILN; contact the
		IMAGE Consortium (info@image.lynl.gov) for further information.
		MGI:146931
		Seq primer: -40RP from Gibco
		High quality sequence stop: 468.
FEATURES	SOURCE	COMMENT
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		/strain="C5BL/6J"
		/db_xref="taxon:10090"
		/clone="IMAGE:3824579"
		/sex="male"
		/issue_type="Thymus"
		/dev_stage="4 weeks"
		/lab_host="DH10B"
		/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
		polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
		was primed with Not I - oligo(dT) primer [5]
		TGTTACCAATCAGAAGGGGACGGCGCTTGTTTTTTTTTTTT
		3]; double stranded cDNA was ligated to Eco RI adaptors
		(Pharmacia), digested with Not I and cloned into the Not I
		and Eco RI sites of the modified pT73 vector. RNA
		provided by Dr. Bertrand Jordan. Library went through two
		rounds of normalization, and was constructed by Bento
		Soares and M. Fatima Bonaldo."
BASE COUNT	ORIGIN	BASE COUNT
186 a	Query Match	32..58;
175 c	Best Local Similarity	Score 641.2; DB 10; Length 702;
182 g	Matches	Pred. No. 2.3e-122;
144 t		Mismatches 8; Indels 2; Gaps 2;
		QY 53 CCAACAAACTGTGCTGTGCTGCTGCCAGCGGGTTCCTGGGCTCTGTGAGTCGAGCCATCA 112
		Db 133 TGCCTATCTCTCTGTGACTATCTGCTCCACTCTTGCTGAGTCGAGCTCCGACATCA 72
		QY 173 CTGCCATCCACTGGCACACTTTCATCTGTAATGGCTAATCCAGTGGTGGAGAG 172
		Db 133 CTGCCATCCACTGGCACACTTTCATCTGTAATGGCTAATCCAGTGGTGGAGAG 192
		QY 233 CACCAAGTGGACATGCCAACATGAGTAGATCCAGTGGCAAAGAGCTATATAACA 292
		Db 193 CACCAAGTGGACATGCCAACATGAGTAGATCCAGTGGCAAAGAGCTATATAACA 252
		QY 293 AACTTTCTGTGCTGCCAGGAAGAGGAGAATGCTCTGGTGCAGATTAAANGA 352
		Db 253 AACATTCTGTGACTCTGCCAACAGAGAGAAATGCTCTGGTGCAGATTAAANGA 312
		QY 353 ATGAACTGGACAGGCTAACAGTCAGTTCCAGAACAGGAAACGGACAGCC 412
		Db 313 ATGAACTGGACAGGTC-AAGCTCAGTTCCAGAACAGGAAACGGACAGCC 371
		QY 413 AGGCATTATCGACACTTACGGACACCCGTGAGAACGGC 472
		Db 372 AGGCATTATCGACACTTACGGACACCCGTGAGAACGGC 431
		QY 473 TACAGAACGCTTAACAGGCGAGATGCTGTGTTCCACCTGAAACAAACATGAAT 532
		Db 432 TACAGAACGCTTAACAGGCGAGATGCTGTGTTCCACCTGAAACATGAAT 491
		QY 533 TCTCGAGGAGCCAGGATGAGCAACAGCTGGGAGGCCACCGACTCAAT 592
		Db 492 TCTCGAGGAGCCAGGATGAGCAACAGCTGGGAGGCCACCGACTCAAT 551
		QY 593 GCAGAGTAAACCATGGAGCAAMTGAATCTCTACTCCAGAGAACCGCTTCAGGTGG 652
		Db 552 GCAGAGTAAACCATGGAGCAAMTGAATCTCTACTCCAGAGAACCGCTTCAGGTGG 611
		QY 653 AGGAGATGATGAGACATGGGTGGGAC-AGTCAGGGTGAGCAGCTGGTGTGAC 711
		Db 612 AGGAGATGATGAGACATGGGTGGGAGCAAGCAGCGGTGGAGCAGCTGGTGTGAC 671
		QY 712 TCGGTTCCCTCAAGAA 729
		Db 672 TCGGTTCCCTCAAGAA 689
		RESULT 6
		BF658170
	LOCUS	BF658170 687 bp mRNA linear EST 20-DEC-2000
	DEFINITION	ma96bb6.y1 soares_thymus 2NbMT Mus musculus cDNA clone IMAGE:3824579 5' similar to TR:008854 008854 TRAF-INTERACTING PROTEIN ;, mRNA sequence.
	ACCESSION	BF658170
	VERSION	BF658170.1 GI:11923304
	KEYWORDS	EST.
	SOURCE	house mouse.
	ORGANISM	Mus musculus
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Qy 496 GAGATCTGTCTCCACCTCGAARACAGATGAAGTCTCTGAGCAGCGCAGGATGAG 555
 Db 481 GAGATCTGTCTCCACCTCGAATAACAGATGAAGTCTCTGAGCAGCGCAGGATGAG 540
 Qy 556 ACCAACAAAGCTCGGGAGGCCACCGACTCAAGTCAAGTCAAACCATGAGCAA 615
 Db 541 ACCAACAAAGCTCGGGAGGCCACCGACTCAAGTCAAGTCAAACCATGAGCAA 600
 Qy 616 ATTGAGCTCTTCACTCGAGGCCACCGACTCAAGTCAAGTCAAACCATGAGCAA 600
 Db 601 ATTGAGCTCTTCACTCGAGGCCACCGACTCAAGTCAAGTCAAACCATGAGCAA 600
 Qy 676 GTGGGACACTCGCCGTTGGAGCAGGT 702
 Db 661 GTGGACAGTCAGCGTGGAGCATGTC 687

RESULT 7
 BF162255 LocusLink ID: BF162255 744 bp mRNA linear EST 30-OCT-2000
 DEFINITION mRNA sequence.
 ACCESSION BF162255
 VERSION EST.
 KEYWORDS house mouse.
 SOURCE Mus musculus.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 744)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://Image.llnl.gov>
 Plate: LLAM9101 row: o column: 12
 High quality sequence stop: 730.
 Location/Qualifiers
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 /strain="CZECH II (feral)"
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 /clone="IMAGE:3990371"
 /clone_id="NCI_CCap_Lu29"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 /stem_cell_origin=""
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pCMV-SPORN6; Site_1: SalI;
 Site_2: Not I; Cloned unidirectionally; Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 BASE COUNT
 ORIGIN
 201 a 183 c 212 g 148 t

RESULT 8
 BM44844 LocusLink ID: BM44844 1061 bp mRNA linear EST 05-FEB-2002
 DEFINITION AGENCOURT 5428661 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5504946
 ACCESSION BM44844
 VERSION BM44844.1 GI:18513886
 KEYWORDS EST.
 SOURCE human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1661)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://Image.llnl.gov>
 Plate: LLAM1217 row: b column: 19
 High quality sequence start: 2

Qy 141 CTCCGACTTCTCGATCACTCCCGTGCCATCCACTCTGGCCACACTTTC 200
 Db 121 CTCCGACTTCTCGATCACTCCCGTGCCATCCACTCTGGCCACACTTTC 180
 Qy 201 TCTGCAATCTCTAATCTGCTTGAGCTGAGCAGCACGTCGGACCTGCCACAGTGTAG 260
 Db 181 TCTGCAATCTCTAATCTGCTTGAGCTGAGCAGCACGTCGGACCTGCCACAGTGTAG 240
 Qy 261 ATCCAGGTGGCAAAGACTATTATAACAACATTCTTGACCTGCCAGGAGA 320
 Db 241 AACAGGTGGCAAAGACTATTATAACAACATTCTTGACCTGCCAGGAGA 300
 Qy 381 TTCCCGAAAGACAGGGACAAAGGGACGCCATATTGACACTTACGGGAC 440
 Db 361 TTCCCGAAAGACAGGGACGCCATATTGACACTTACGGGAC 420
 Qy 441 CCTGGAGAACGCATCTACCGTGGAGTCCCTACAGAACGCCCTAACAGGCAGAG 500
 Db 421 CCTGGAGAACGCATCTACCGTGGAGTCCCTACAGAACGCCCTAACAGGCAGAG 360
 Qy 501 GCTGTGTCACCCGTGAAACAGATGAGTCTCTGGAGCAGCGCAGAGCAA 560
 Db 481 GCTGTGTCACCCGTGAAACAGATGAGTCTCTGGAGCAGCGCAGAGCAA 540
 Qy 561 ACAAGCTCGGAGGAGGCCACCGACTCAAGTCAAGTCAAACCATGGAGCAAATG 620
 Db 541 ACAAGCTCGGAGGAGGCCACCGACTCAAGTCAAGTCAAACCATGGAGCAAATG 598
 Qy 621 GCTCTACTCCAGGCCACGCTCTGAGGGAGGATGATGAGACATGGTGTGG 680
 Db 599 GCTCTACTCCAGGCCACGCTCTGAGGGAGGATGATGAGACATGGTGTGG 658
 Qy 681 ACAGTCAGGGTGGAGCAGCTGGTGTACTCGGTGTCCTCAAGRAAGAGTATGAGA 740
 Db 659 ACAGTCAGGGTGGAGCAGCTGGTGTACTCGGTGTCCTCAAGRAAGAGTATGAGA 715
 Qy 741 TCTGAAGGA 749
 Db 716 TTGAGGAA 724

FEATURES source	High quality sequence stop: 641. Location/Qualifiers
1. .1061	
/organism="Homo sapiens"	
/lab_xref="IMDB:5304946"	
/clone="IMACB:5304946"	
/clone_1b="NIH_MGC_85"	
/tissue_type="lymphoma, cell line"	
/lab_host="DH10B (phage-resistant)"	
/note="Organ: lymph; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."	
BASE COUNT	282 a 272 c 297 g 202 t 8 others
ORIGIN	
Query Match	30.5%; Score 603; DB 10; Length 1061;
Best Local Similarity	80.4%; Pred. No. 1.7e-114;
Matches	605; Conservative 0; Mismatches 106; Indels 2; Gaps 2;
QY	81 TGGTTCCCTGGGAGCTGAGTGAGGCCATCATGCCCTACCTCCTCTGTGACTATCTG 140
Db	64 TGGCTGCCGGGCCCTTGAGTCAGCCATCATGCCCTACCTCCTCTGTGACTATCTG 123
QY	141 CTCGCACTCTTGTGATCACTCCCGTGAAGCTGGTGGCGCCATCCACTGTGGCACATTTCGA 200
Db	124 CTCGCACTCTGATCACTCCCGCAGCTGGCGCCATCCACTGTGGGCCACCTTCGA 183
QY	201 TCGCACTGCTTAATCCAGTGGTGAACAGACCAAGTCGACGCCATCCAGTGGAG 260
Db	184 CTTCAGCTGCTTAATTCAGTGGTGAACAGACCAAGTCGACGCCAGTGGCG 243
QY	261 ATCCAGGTGGGAAAGAACATAATTAAACAACTTCTTGACCTCGCCAGGAAGA 320
Db	244 ATTCAGGTGGGAAAGAACATTATCAATAGCTCTTGTGACCTCGCCAGGAAGA 303
QY	321 GGAGAATGCTTGTGAGAAATCTTAAAGAAGAATCTGGAGACGGCTCAACCTCACT 380
Db	304 GGAGAATGCTGATGAGAACATCTTAAGAATGAATGAGAACATGGACATGTCAGAGCCCAGCT 363
QY	381 TTCCAGAAAGAGAGGGAAAGGGAGGCCATTAGGACACTCTAGGGCAC 440
Db	364 TTCCAGAAAGAGCAAGAGAACAGACGCCATGACACTCTGGGGATAC 423
QY	441 CCTGGAAGAACGATGCTACCTGGTCCATAGACGCCATTAACAAAGGGAGAT 500
Db	424 GCTGGAAGAACGATGCTACCTGGTACCTCGCAGAGGCCCTGGCAAGGCCAGAT 483
QY	501 GCTGTGTTCACCTGAAAGAACGATGAGTCTGGAGCACGGAGGATGACCAA 560
Db	484 GCTGTGTCACACTGAAGAACGATGAGTACTTAGAGCAGCAGATGACCAA 543
QY	561 ACAGAGCTGGAGAGGCCACCGACTCAAGTGAAACCATGGACAAATGCA 620
Db	544 ACAGACACAGAGGAGGCCGGCGCTCAGGACAAAGTGAGAACGATGAGATGCA 603
QY	621 GCTCTACTGAGGCCAGCGTCTGAGGTGGAGGAGATGAGATGAGATGAGATGAGA 680
Db	604 GCTCTACTGAGGCCAGCGTCTGAGGTGGAGGAGATGAGATGAGATGAGATGAGA 663
QY	681 ACTCTCAGGGTGAGCACTGCTGTGACTCTGGTCCCTGAGAAAGAGATGAGAA 740
Db	664 ACAGTCAGGGTGAGACGCTGCTGTACTGTGCTCTGAGAAGAGATGAGAA 723
QY	741 TCTGAAGGAGCTGGAGGCCAGGGAGACTGGCTGAGAGCTGGAGAAGGATGGT 800
Db	724 TCTANAAAGGAGCAGGAGGCCCTCAGGGAGGTGCTGAGAAGAGATGAGATGAGA 783
QY	801 GTCC-TCTAGGAGCAAGTGAAGACTCTCAACACTGAGCTGGTCAAGGCCAAG-TTGA 858
Db	784 TTCCNTCCAGAAGSCAAGNTGCAAGACAGCTACTCTGAATTGGATCAAGGCCAGTTAGAA 843
RESULT	9
BIG96519	
LOCUS	BIG96519 608 bp mRNA linear EST 18-SEP-2001
DEFINITION	603347473F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5374770 5'
SOURCE	mRNA sequence.
ACCESSION	BIG96519
VERSION	BIG96519.1 GI:15659148
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murine; Mus.
AUTHORS	1 (bases 1 to 608)
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs@nlm.nih.gov
TISSUE	Procurement: Gilbert Smith, Ph.D.
CDNA LIBRARY	Preparation: Life Technologies, Inc.
DNA SEQUENCING	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (L1NL)
Clone distribution	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/L1NL at: http://image.llnl.gov
http://image.llnl.gov	
Plate:	LLAM1954
Row:	b
Column:	19
High quality sequence stop:	605.
Location/Qualifiers	
1. .608	
/organism="Mus musculus"	
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/lab_xref="Taxon:1090"	
/clone="IMACB:534770"	
/clone_1b="NCI_CGAP_Mam2"	
/tissue_type="tumor, biopsy sample"	
/dev_stage="5 months"	
/lab_host="DH10B"	
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"	
FEATURES source	
BASE COUNT	155 a 152 c 159 g 141 t 1 others
ORIGIN	
Query Match	28.8%; Score 568.2; DB 10; Length 608;
Best Local Similarity	98.9%; Pred. No. 2.8e-107;
Matches	603; Conservative 0; Mismatches 4; Indels 3; Gaps 3;
QY	1251 GGAACCTGGTGTGCTCCCTCTCTGATCCGGAAATGGTCTGGTCAAGAACGCC 1310
Db	1 GGAACCTGGTGTGCTCCCTCTGATCCGGAAATGGTCTGGTCAAGAACGCC 60
QY	1311 CAACAGGACACACAGATGCCGAAGAGCACAGATGGTGAAGATAGGCTTGTGG 1370
Db	61 CAACAGGACACACAGATGCCGAAGAGCACAGATGGTGAAGATAGGCTTGTGG 119
QY	1371 GCTTGGAGGAGCAAGAACATTCACTGCCCTAGGGACACAACTTATCCGACGCC 1430
Db	120 GCTTGGAGGAGCAAGAACATTCACTGCCCTAGGGACACAACTTATCCGACGCC 179
QY	1431 TGTAACTGCCAGGAGCAAGTAAAGAGAGATGAGTCTGGCTC 1490
Db	180 TGTTAAGTCGAAGGCCAAGAGTAAACAGAAAGTGGAGATAAGCTGGAGTCTGCCTC 239
QY	1491 CCASCCCAAGCTGGATACCTCTTATGTCAGTGAACGGTGGACAGAGTGTGCAAT 1550

			NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
Db	240	CCAGGCCAACCTGGATACCTCTTATGTCAGTGACGGTGACAGAGTCATGTTGCAAT	299
Qy	1551	TAGTGGGCCAAGACCTGGCTAACCGAAGGTGTTTGGAGATGSGCTCCCTTGACCG	1610
Db	300	TAGTGGGCCAAGACCTGGCTAACCGAAGGTGTTTGGAGATGSGCTCCCTTGACCG	358
Qy	1611	TCCAGAGAGATGCCAGAAAACACTTCTGTTCACTGGCCCTGCACACACTGG	1670
Db	359	TCCAGAGAGATGCCAGAAAACACTTCTGTTCACTGGCCCTGCACACACTGG	418
Qy	1671	G-AAGCCACATGACCAGTTACTGTTCCAGTCAGGGCCTACTTCAGTGAGGGT	1729
Db	419	GAAAGCCACATGACCAGTTACTGTTCCAGTCAGGGCCTACTTCAGTGAGGGT	478
Qy	1730	TTGCTTATAGCTACACCAGGTGTTGCTGACTCTTGTATAGACAGGGTAC	1789
Db	479	TTGCTTATAGCTACACCAGGTGTTGCTGACTCTTGTATAGACAGGGTAC	538
Qy	1790	ATGACTCTAGTGGATGCTGGAGATCCTATCAGGCTGGGCT 1849	
Db	539	ATGACTCTAGTGGATGCTGGGAGATCCTATCAGGCTGGGCT 598	
Qy	1850	TGACTCTCG 1859	
Db	599	TGAACCTCTG 608	
RESULT	10		
LOCUS	BE334637		
DEFINITION	usb1912.y1 NCI-CAP_Mm4 Mus musculus mRNA clone IMAGE:3257638 5'		
ACCESSION	BE334637		
VERSION	1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 599)		
AUTHORS	NCI-CAP http://www.ncbi.nlm.nih.gov/ncicicap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Straubnberg, Ph.D. Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth Ph.D. DNA library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: NCI-CAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml image.llnl.gov/image/html/iresources.shtml MGI:1069002		
FEATURES	High quality sequence stop: 362.		
source	Location/Qualifiers		
1.	.589		
/organism="Mus musculus"			
/strain="NMR1"			
/db_xref="taxon:10090"			
/clone="IMAGE:3257638"			
/clone_id="NCI-CAP_Mm4"			
/tissue_type="tumor, gross tissue"			
/dev_stage="5 months"			
/lab_host="BHLB"			
/note="Organ: mammary; Vector: PCMV-SPORT5; Site 1: Sali; Site 2: NotI; Cloned unidirectionally; Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth,"			
RESULT	11		
LOCUS	AA684194		
DEFINITION	AA684194 vms8d10.s1 Knowles Solter mouse 2 cell 1 mus musculus mRNA clone IMAGE:10034115, similar to TR:008854 008854 MTRP. ;, mRNA sequence.		
ACCESSION	AA684194		
VERSION	AA684194.1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 554)		
AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubroque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellebenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterton, R.		
TITLE	The WashU-HMM Mouse EST Project		
COMMENT	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project		

		Db	546	TGCAGATG		Mouse EST Project
						Washington University School of Medicine
						4444 Forest Park Parkway, Box 5501, St. Louis, MO 63108
						TEL: 314 286 1800
						FAX: 314 286 1810
						Email: mouseest@watson.wustl.edu
						This clone is available royalty-free through LLNL; contact the IMAGE Consortium (http://image.llnl.gov) for further information.
						MGID:567627
						Possible reversed clone: similarity on wrong strand
						High quality sequence stop: 512.
FEATURES	source	LOCATION/QUALIFIERS				
		1. . .554				
		/organism="Mus musculus"				
		/strain="B6D2 Flv/J"				
		/db_xref="taxon:10090"				
		/clone=IMAGE:1003411"				
		/clone.lib="Knowles Solter mouse 2 cell"				
		/tissue_type="embryo"				
		/dev_stage="2-cell"				
		/lab_host="DH110B"				
		/note="organ: embryo; vector: bluescribe (modified); site_1: MuRI; site_2: Sali; cloned unidirectionally from mRNA prepared from 13-500 2-cell stage embryos. Primer: Sali(dT); 5'-CGTGACGCTGACGCTGTTTGTGTTTGTGTTT-3'. cDNAs were cloned into the MuRI/Sali sites of a modified bluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."				
BASE COUNT		149 a 151 c 139 g 115 t				
ORIGIN						
FEATURES	source	LOCATION/QUALIFIERS				
		Best Local Similarity 99.3%; Pred. No. 7.8e-100; Mismatches 545; Conservative 0; Indels 1; Gaps 1;				
QY	53	CCACCAAAGTGTGTCGTCGTCGAGCAGTCAGCTTCCTGGCTCTTGACTCGGCCATCA	112			
Db	6	CCACCAAAGTGTGTCGTCGTCGAGCAGTCAGCTTCCTGGCTCTTGACTCGGCCATCA	65			
QY	113	TGCCATTATCCCTCTCTGTGACTCTGTCTCCGACTCTCTGATCACTCCGTGAGCTG	172			
Db	66	TGCCATTATCCCTCTCTGTGACTCTGTCTCCGACTCTGTCTCCGTGAGCTG	125			
QY	173	CTGCATCCACTGTGCGCACACTTTCATCTGCAATGCCATTACAGTGGTTAGACAG	232			
Db	126	CTGCCATCCACTGTGCGCACACTTTCATCTGCAATGCCATTACAGTGGTTAGACAG	185			
QY	233	CACCAAGTGGACCTGCCAACAGTAGATCAGTCAGTGGCAAAAGACTTATAACA	292			
Db	186	CACCAAGTGGACCTGCCAACAGTAGATCAGTCAGTGGCAAAAGACTTATAACA	245			
QY	293	ACCTTTCTTTCGACCTGCCAACAGAGAGAATGTCAGTCAGATCTTAAGA	352			
Db	246	ACCTTTCTTTCGACCTGCCAACAGAGAGAATGTCAGTCAGATCTTAAGA	305			
QY	353	ATGAACTGGACAGCTCAAGCTAGCTTCCCGAAAGACAGGAGAACGGGACAGCC	412			
Db	306	ATGAACTGGACAGCTCAAGCTAGCTTCCCGAAAGACAGGAGAACGGGACAGCC	365			
QY	413	AGGCATTATGACACTCTAGGACACCTGTGAGAAGACGCAAGCTACGGTGTGTC	472			
Db	366	AGGCATTATGACACTCTAGGACACCTGTGAGAAGACGCAAGCTACGGTGTGTC	425			
QY	473	TACAGAACGCTTAACAAAGCAGAGATGCTGTGTTCCACCT-GAAAACAGATGAG	531			
Db	426	TACAGAACGCTTAACAAAGCAGAGATGCTGTGTTCCACCT-GAAAACAGATGAG	485			
QY	532	TTCTTGAGGAGCGCCAGGTGAGACCAACAACTGCTGGAGGAGGCCACCGACTCAAG	591			
Db	486	TTCTTGAGGAGCGCCAGGTGAGACCAACAACTGCTGGAGGAGGCCACCGACTCAAG	545			
QY	592	TGCAAGATG	600			
FEATURES	source	LOCATION/QUALIFIERS				
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		/strain="B6D2 Flv/J"				
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		/clone.lib="Knowles Solter mouse 2 cell"				
		/tissue_type="embryo"				
		/dev_stage="2-cell"				
		/lab_host="DH110B"				
		/note="organ: embryo; vector: bluescribe (modified); site_1: MuRI; site_2: Sali; cloned unidirectionally from mRNA prepared from 13-500 2-cell stage embryos. Primer: Sali(dT); 5'-CGTGACGCTGACGCTGTTTGTGTTTGTGTTT-3'. cDNAs were cloned into the MuRI/Sali sites of a modified bluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."				
BASE COUNT		149 a 151 c 139 g 115 t				
ORIGIN						
FEATURES	source	LOCATION/QUALIFIERS				
		Best Local Similarity 99.3%; Pred. No. 7.8e-100; Mismatches 545; Conservative 0; Indels 1; Gaps 1;				
QY	81	TGGTTCCTGGCGCTTGAGTCAGCCACATGCCATATCTCTCTCTGACTATCTG	140			
Db	42	TGGCTCCCTGGGCCCTTGAGTCAGCCATCATGCCATATCTCTCTGACTATCTG	101			
QY	141	CTCCGACTCTTCGTCATCCCTGGAGCCACCTGGCCACACTTGCGCACACTTTC	200			
Db	102	CTCCGACTCTTCGTCATCCCTGGAGCCACACTTGCGCACACTTTC	161			
QY	201	TCTGCAATGCTTAACAAAGCAGAGATGCTGTGTTCCACCT-GAAAACAGATGAG	260			
Db	162	CTTGGAGTGGCTTAACAAAGCAGAGATGCTGTGTTCCACCT-GAAAACAGATGAG	221			
QY	261	AATCCAGGTGGCAAAAGACTATATAACAACTTTCCTTGACCTGCGCCAGGAAGA	320			
Db	222	AATCCAGGTGGCAAAAGACCATATCATATAACCTGCTCTTGTGTCAGGAGG	281			
QY	321	GGAGATGTTGGATGCGAATCTTAAGAATGAACTGGACAGCGTCAGCTCAGGT	380			

Best Local Similarity 84.5%; Pred. No. 5.2e 96'; Matches 612; Conservative 0; Mismatches 109; Index 3; Gaps 3;

Db	282 GGAGAAATGTCCTGGATGCAGAATTCATAAGAATGACTGGACAGAATGTCAGGCCAGT 341
Oy	381 TTCCCGAAGAACGAGACGGAGAACGGGACAGCCAGGCAATTATCGACACTCTACGGACAC 440
Db	342 TTCCCGAAGAACGAGACGGAGAACGGGACAGCACTGCGCATC 401
Oy	441 CCTGGAGAACGCAATGCTACGGTAGCTCCATAGAAAGCCTTAACAGAGAGAT 500
Db	402 GCTGGAAAGACGCAATGCTACTGTGATTCCTGGAGCHGCGCTGGCAAGGCCAGAT 461
Oy	501 GCTGTTTCTCACCTGAAGAACAGATGAATGCTTGAGSCAGCGCAGGATGACCAA 560
Db	462 GCTGTTCTCACCTGAAGAACAGATGAATGCTTGAGSCAGCGCAGGATGACCAA 521
Oy	561 ACAAAGCTGGAGGGGCCACCGACTCAAGTCAAGTGAATGAAACCATGAGAACATTGA 620
Db	522 GCAAGACAAGGGAGGCCGCGCTCAAGCAGATGAGAACATGAGCATGAGATGAGATGA 581
RESULT	13
Db	BGG82548
LOCUS	BGG82548
DEFINITION	603624362f1 NCI_CGAP_Skn4
mRNA sequence.	
ACCESSION	582 GCTCTTACTCGAGGCCAGGCCUCGAGGAGCACGATGTCGGAGACATGGGTGTTG 641
VERSION	EST.
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	1 (bases 1 to 752)
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
COMMENT	Unpublished (1999)
Contact:	Robert Strausberg, Ph.D.
Tissue Procurement:	James Cleaver, M.D.
cDNA Library Preparation:	Life Technologies, Inc.
cDNA Library Arrayed by:	the T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:	Incyte Genomics, Inc.
Clone distribution:	MGC clone distribution information can be found through the T.M.A.G.E. Consortium at: http://image.llnl.gov
Plate:	LIAM10602 row: k column: 16
High quality sequence start:	19
High quality sequence stop:	736.
FEATURES	source
1. . 752	/organism="Homo sapiens"
/db_xref="taxon:9606"	/clone="IMAGE:474947"
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/lab_host="DH10B (T1 phage-resistant)"	/note="Organ: skin; vector: pCMV-SPORE6; Site_1: NOTI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT	200 a 194 C 212 G 146 T
ORIGIN	
Query Match	26.0%; Score 513.6; DB 10; Length 752;

Db	291 CAACATTCTTGACTCGCCAGGAGAATGTTGGATGCAATTCTAA 350
Oy	471 CCTACAGAGCCCTAACAGGGAGATGCTGTCACCTGAAACAGATGMA 530
Db	447 TCTGCAGCAGGCCCTGGCAGGGCAGATGCTGTCACCTGAAACAGATGAA 506
Oy	531 GTTCCTGGACAGCGCAGATGAGACCAACAACTGCTGGAGGAGGCCACCGACTAA 590
Db	507 GTACTTAGCAGCAGCAGCTGCGATCTGCAGTC 446
Oy	591 GTGCAGAGAAACCATGAGCAATTCAGCTCTACTCCAGGCCAGGAGTCAG 650
Db	627 GGAGGAGATGAGCACATGAGATGAGATGAGCTCTACAGGCCAGGAGTCAG 686
Oy	651 GGAGGAGATGAGCAATGGGTGAGCAGTCAGCTGGTGG-AGCAGCTGGCTGT 709
Db	710 ACTGGGTGCTCT-CAAGAAAGATGATGAGATCTGAAGGAAGCTGGAGGCCACAGG 768
Oy	687 ACTGTTGCTCTCCAAAGAAAGATGAGCAATCTAAAGAGGCCGGAGGCCGG 746
Db	769 GAAC 772
Oy	747 GCAC 750
RESULT	14
Db	BE304189
LOCUS	BE304189
DEFINITION	60108621f1 NCI_CGAP_Mam6
mRNA sequence.	
ACCESSION	BE304189
VERSION	BE304189.1 GI:9174333
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 519)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
Contact:	Robert Strausberg, Ph.D.

	DEFINITION	602347389F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4442038 5'
	TISSUE	mRNA sequence.
	PROCUREMENT	Jeffrey Green M.D.
	LIBRARY PREPARATION	Life Technologies, Inc.
	CDNA LIBRARY ARRAYER	The I.M.A.G.E. Consortium (LNL)
	DNA SEQUENCING BY	Incyte Genomics, Inc.
	Clone distribution by	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
FEATURES	source	Plate: LLAM059 row: i column: 06
		High quality sequence stop: 515.
		Location/Qualifiers
BASE COUNT		1. .519
ORIGIN		/organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:3500621" /clone.lib="NCICBAP.Mam6" /sex="female" /tissue_type="infiltrating ductal carcinoma" /dev_stage="5 months" /lab_host="DH10B" /note="Organ: mammary; Vector: pcMV-SPORT6; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
Query Match		26.0%; Score 513.4; DB 10; Length 519;
Best Local Similarity		99.8%; Pred. No. 6e-95; Mismatches 0; Gaps 0;
Matches		514; Conservative 0; Indels 0; Gaps 0;
Qy	263	TCCAGGTGCAAAAGACTATATAAACAAACCTTCTGGCTCGCCAGAAGAGG 322
Db	5	TCCAGGTGCAAAAGACTATATAAACAAACCTTCTGGCTCGCCAGAAGAGG 64
Query Match		26.0%; Score 513.4; DB 10; Length 519;
Best Local Similarity		99.8%; Pred. No. 6e-95; Mismatches 0; Gaps 0;
Matches		514; Conservative 0; Indels 0; Gaps 0;
Qy	323	AGAATGTCCTGGATCAGATTCTAACAGATGACTGGACAGGGTCAAAGCTAGCTT 382
Db	65	AGAATGTCCTGGATCAGATTCTAACAGATGACTGGACAGGGTCAAAGCTAGCTT 124
Query Match		26.0%; Score 513.4; DB 10; Length 519;
Best Local Similarity		99.8%; Pred. No. 6e-95; Mismatches 0; Gaps 0;
Matches		514; Conservative 0; Indels 0; Gaps 0;
Qy	383	CCAGAAAGCAGGGAGAACGGCACGCCATTATCGACACTCTACGGACACCC 442
Db	125	CCAGAAAGCAGGGAGAACGGCACGCCATTATCGACACTCTACGGACACCC 184
Query Match		26.0%; Score 513.4; DB 10; Length 519;
Best Local Similarity		99.8%; Pred. No. 6e-95; Mismatches 0; Gaps 0;
Matches		514; Conservative 0; Indels 0; Gaps 0;
Qy	443	TGGAAGAAGCAATCTACGGTAGCTAACAGCAGGAGATGACCTCTACGGACACC 502
Db	185	TGGAAGAAGCAATCTACGGTAGCTAACAGCAGGAGATGACCTCTACGGACACC 244
Query Match		25.9%; Score 510.6; DB 10; Length 784;
Best Local Similarity		87.2%; Pred. No. 2.2e-95; Mismatches 84; Gaps 3;
Matches		594; Conservative 0; Indels 3; Gaps 3;
Qy	81	TGGTCCCCGGCCTTGATGAGCCATCATGCCTATCTCTCTGGCACTATCTG 140
Db	62	TGGTCCCCGGCCTTGATGAGCCATCATGCCTATCTCTGGCACTATCTG 121
Query Match		25.9%; Score 510.6; DB 10; Length 784;
Best Local Similarity		87.2%; Pred. No. 2.2e-95; Mismatches 84; Gaps 3;
Matches		594; Conservative 0; Indels 3; Gaps 3;
Qy	503	TGTGTCCACCCGAAACAGATGAGTCTGGAGGAGGGTGGAGACCAAC 562
Db	245	TGTGTCCACCCGAAACAGATGAGTCTGGAGGAGGGTGGAGACCAAC 304
Query Match		25.9%; Score 510.6; DB 10; Length 784;
Best Local Similarity		87.2%; Pred. No. 2.2e-95; Mismatches 84; Gaps 3;
Matches		594; Conservative 0; Indels 3; Gaps 3;
Qy	563	AAGCTGGGGAGGCCACCGCACTCAAGTGCAAGATGAAACCATGGAGCAATTGASC 622
Db	305	AAGCTGGGGAGGCCACCGCACTCAAGTGCAAGATGAAACCATGGAGCAATTGASC 364
Query Match		25.9%; Score 510.6; DB 10; Length 784;
Best Local Similarity		87.2%; Pred. No. 2.2e-95; Mismatches 84; Gaps 3;
Matches		594; Conservative 0; Indels 3; Gaps 3;
Qy	623	TCTRACTCGAGAGCAGCGTCTCAGGAGGAGATGAGACATGGGGTGGGAC 682
Db	365	TCTRACTCGAGAGCAGCGTCTCAGGAGGAGATGAGACATGGGGTGGGAC 424
Query Match		25.9%; Score 510.6; DB 10; Length 784;
Best Local Similarity		87.2%; Pred. No. 2.2e-95; Mismatches 84; Gaps 3;
Matches		594; Conservative 0; Indels 3; Gaps 3;
Qy	683	AGTCAGGGGGAGCAGCTGGTACTGGCTCTCAAGAAAGACTATGAGATC 742
Db	425	AGTCAGGGGGAGCAGCTGGTACTGGCTCTCAAGAAAGACTATGAGATC 484
Query Match		25.9%; Score 510.6; DB 10; Length 784;
Best Local Similarity		87.2%; Pred. No. 2.2e-95; Mismatches 84; Gaps 3;
Matches		594; Conservative 0; Indels 3; Gaps 3;
Qy	743	TGAAGGAAGCTGGAGGACACAGGGAAACTGTCT 77
Db	485	TGAAGGAAGCTGGAGGACACAGGGAAACTGTCT 519
RESULT	15	BG120736
LOCUS		784 bp mRNA linear EST 30-JAN-2001

QY 501 GCTGCGTGTCCACCCGTGAAAAAACAGATGAAGTCTGGCGAGGGCAGTAGACCA 560
 Db 1 GCCCCCTTGAGTCAGCCATCATGCCTATCGTGTCTGCACTTCAGTCAGTC 60
 Db 482 GCTGTCCTCACACTGAAAGCAGATGAATCTAGAGCAGCAGCAGGATGACCA 541
 QY 561 ACAAAGCTGGAGGGCCACCGACTCAAGTCAGTGCAGATGAACCATGGAGAATGA 620
 Db 542 ACAAAGCAAGAGGGGCC-GCGCTCTAGAGCAAGATGAAGACATGGAGCAGATTGA 600
 QY 621 GCTCCCTACTCGAGGCCAGGGTCTGAGGGAGGAGATGATTCCAGACATGGGGTGG 680
 Db 601 GCTTCTACTCCAGGCCAGGCCCTGAGGAGATGATCCGAGACATGGTGGGG 660
 QY 681 ACAGTCAGCGGGGGCAGCTGGCTGAGTGGCTCTAGAAGAGATGAGAA 740
 Db 661 ACAGTCAGCGGGAGGCCAGCGCTG-TGTGACTGTCGTCCTCCAGAAAGAT-CGAAA 718
 QY 741 TCTGAGGAGGCTCGGAAGGC 761
 Db 719 TCTAAAGAAGCCGGAGGCC 739

RESULT 16
 LOCUS BG420765
 DEFINITION 602448558F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4586846 5',
 ACCESSION BG420765
 VERSION BG420765.1 GI:13327271
 KEYWORDS EST.
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 ORGANISM Homo sapiens
 REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC <http://mgc.ncbi.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 TISSUE Procurement: bcdP/dtp
 DNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Email: cgabps-r@mail.nih.gov
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://Image.llnl.gov>
 plate: LIML316 row: d column: 15
 High quality sequence stop: 719.
 FEATURES source
 /clone="IMAGE:4586846"
 /clone_ib="NIH_MGC_14"
 /tissue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: kidney; Vector: pCRB7; Site_1: XbaI; Site_2:
 ECORI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XbaI sites using the following,
 adaptor: GGACGG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT a 229 c 274 g 170 t
 ORIGIN

RESULT 17
 LOCUS BE546959
 DEFINITION 60107129F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:34588023 5',
 ACCESSION BE546959
 VERSION BE546959.1 GI:9775604
 KEYWORDS EST.
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Query Match 25.5%; Score 504.2; DB 10; Length 908;
 Best Local Similarity 82.0%; Pred. No. 4.4e-94;
 Matches 663; Conservative 0; Mismatches 93; Indels 53; Gaps 5;
 QY 91 GGCTGCTGAGTCGAGCCATCATGCCTATCCTCTCTGCACTATGCTCCGACTTC 150

	BASE COUNT	163 a	171 c	172 g	126 t
Db	303	GGAGAATGCTTGGATGCAGAAATTAAAGAATGAACTGGACATGTCAAGGCCAGT	362		
Qy	381	TCCCCAGAAGAACAGGGAGAACGGACACGCCGCCCCATPATCGAACACTCTACCGGACAC	440		
Db	363	TCCCCAGAAGAACAGGGAGAACGGACACGCCGCCCCATPATCGAACACTCTACCGGATAC	422		
Qy	441	CCTGAAAGAACGCAATGCTACCGTGAGTCCTACAGAACGCCATTAAACAAAGCAGAT	500		
Db	423	GCTGGAGAACGCAATGCTACCGTGAGTCCTACAGAACGCCATTAAACAAAGCAGAT	482		
Qy	501	GCTGTTCCACCTGAAGAACAGATGAGTCCTGGACCGAGGGCAGGATGAGCAA	560		
Db	483	GCTGTTCTCACACTGAAGAACAGATGAGTCCTGGACCGAGGGCAGGATGAGCAA	542		
Qy	561	ACAACTGGAGGGGCCACCGACTCAAGTGAAGAACCATGGACAAATTGA	620		
Db	543	ACAACTGGAGGGGCCACCGACTCAAGTGAAGAACCATGGACAAATTGA	602		
Qy	621	GCTCTACTTCAGGCCACGGTGTGAGTGGAGGAGATCGAG-ACATGGTGG	679		
Db	603	GCTCTACTTCAGGCCACGGTGTGAGTGGAGGAGATCGAG-ACATGGTGG	651		
Qy	680	GACAGTCACGGGGACCGCTGCTGGTAAAGGGGCTCTCAAGAAAGGTC	738		
Db	662	GACAGTCACGGGGACCGCTGCTGGTAAAGGGGCTCTCAAGAAAGGTC	721		
Qy	739	AATCTGAAGGAAGCTCGGAGGCCA	763		
Db	722	AATCCAAAGAGGCCGAAGCTCA	746		
RESULT	22				
BF219707					
LOCUS		632 bp mRNA linear EST 08-NOV-2000			
DEFINITION		60129627FE NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821007 5'			
ACCESSION		mrNA sequence.			
VERSION		BP219707			
KEYWORDS		EST.			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 632)			
AUTHORS		NIH-MGC http://mgc.ncbi.nih.gov/			
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL		Unpublished (1999)			
COMMENT		Contact: Robert Strausberg, Ph.D.			
CDNA Library Arrayed by:		The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by:		Incyte Genomics, Inc.			
Clone distribution:		MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			
Plate:		IRALI row: e column: 07			
High quality sequence stop:		630.			
FEATURES		Location/Qualifiers			
source		I.. .632			
/organism="Homo sapiens"					
/clone="IMAGE:2821007"					
/clone_lib="NIH MGC_7"					
/tissue_type="small cell carcinoma"					
/cell_line="MGC3"					
/lab_host="PH10B (phage-resistant)"					
Note="Organ: lung; Vector: POMB7; Site_1: XbaI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adapter: GCGCGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."					
RESULT	23				
BG117979					
LOCUS		912 bp mRNA linear EST 30-JAN-2001			
DEFINITION		60235123F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:446149 5'			
ACCESSION		mrNA Sequence.			
VERSION		BG117979			
KEYWORDS		EST.			
SOURCE		human.			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 912)			
AUTHORS		NIH-MGC http://mgc.ncbi.nih.gov/			
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL		Unpublished (1999)			
COMMENT		Contact: Robert Strausberg, Ph.D.			
Email: cgabbs@mail.nih.gov					
Tissue Procurement:		ATCC			
CDNA Library Preparation:		Life Technologies, Inc.			
CDNA Library Arrayed by:		The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by:		Incyte Genomics, Inc.			
Clone distribution:		MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:			

		RESULT	24
FEATURES	source	BB821649	BB821649
High quality sequence stop	678.	LOCUS	BB821649 RIKEN full-length enriched, mammary gland RCB-0526
Location/Qualifiers	1. . 912	DEFINITION	JYg-MCA) cDNA Mus musculus cDNA clone G830012P09 3', mRNA sequence.
/organism="Homo sapiens"		ACCESSION	BB821649
/db_xref="txon:9606"		VERSION	BB821649.1 GI:16994278
/clone="IMAKE:446149"		KEYWORDS	EST.
/clone.lib=NIH_MGC_90"		SOURCE	house mouse.
/tissue_type="adenocarcinoma, cell line"		ORGANISM	Mus musculus
/lab_host="PhLB0 (phase-resistant)"		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; MUS.
/note="organ: liver; vector: pcMV-SPORT6; site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.		REFERENCE	1 (bases 1 to 528)
Note: this is a NIH_MGC library."		AUTHORS	Akimura,T., Arkawa,T., carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomatsu,R., Okazaki,T., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takagi,Akira,S., Tanaka,T., Tomaru,T., Toya,T., Watanuki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
BASE COUNT	ORIGIN	TITLE	RIKEN Encyclopedia of Mouse Full-Length cDNAs (Akimura,T., et al. 2001)
236 a 243 c 273 g 160 t		COMMENT	Unpublished (2001)
Query Match	23 3%	PREDICTED	Contact: Yoshihide Hayashizaki
Best Local Similarity	83.8%	PRED.N.	Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
Matches	591	INDELS	The Institute of Physical and Chemical Research (RIKEN)
Conservative	0	GAPS	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
		JOURNAL	Tel: 81-45-503-9222
		COMMENT	Fax: 81-45-503-9216
		PREDICTED	Email: genome-res@gsc.riken.go.jp/
		PRED.N.	URL: http://genome.gsc.riken.go.jp/
		INDELS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
		GAPS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
		JOURNAL	wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
		COMMENT	RIKEN Integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
		PREDICTED	Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
		PRED.N.	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-299 (2001)
		INDELS	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
		GAPS	e mouse tissues.
FEATURES	LOCATION/QUALIFIERS	LOCATION/QUALIFIERS	LOCATION/QUALIFIERS
		1. . 528	1. . 528
	/organism="Mus musculus"	/db_xref="taxon:10090"	/db_xref="taxon:10090"
	/clone="G830012P09"	/clone.lib="RIKEN full-length enriched, mammary gland RCB-0526 JYg-MC(A) cDNA"	/clone.lib="RIKEN full-length enriched, mammary gland RCB-0526 JYg-MC(A) cDNA"
	/tissue_type="mammary gland"	/cell_line="RCB-0526 JYg-MC(A)"	/cell_line="RCB-0526 JYg-MC(A)"
BASE COUNT	ORIGIN	BASE COUNT	BASE COUNT
137 a	ORIGIN	137 a	137 a
121 c		117 g	117 g
153 t		153 t	153 t
Query Match	22 1%	PREDICTED	Length 528;
Best Local Similarity	93.2%	PRED.N.	Length 528;
Matches	490	INDELS	Length 528;
Conservative	0	GAPS	Length 528;
		JOURNAL	Length 528;
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		PREDICTED	Length 528;
		PRED.N.	Length 528;

FEATURES	source	BASE COUNT	ORIGIN	Locus	DEFINITION	ACCESSION	VERSION
sequencing pipeline with 384 multicapillary sequencer.				AZ406449	Mouse 10kb plasmid UGGC1M library	IM0175M08	519 bp DNA linear GSS 03-OCT-2000
Genome Res. . 10 (10), 1617-1630 (2000)					Mus musculus genomic sequence.		
wagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.							
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline							
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library.							
Genome Res. . 11 (2), 281-289 (2001)							
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.							
e mouse tissues.							
Location/Qualifiers							
1. . 519							
/organism="Mus musculus"							
/db_xref="taxon:10090"							
/clone_id="RICK0002K10"							
/clone_lib="RIKEN full-length enriched, Nullipotent stem cell CRL-2070 NE cDNA"							
/cell_line="CRL-2070 NE"							
base count		126	a	116	b	136	g
origin				141	t		
Query Match		21.8%		Score 430; DB 9;		Length 519;	
Best Local Similarity		94.9%		Pred. No. 1e-78;			
Matches		488;	Conservative	0;	Mismatches		
Qy	1444	GCCAGAGTAAACAGAAAGGAGATAAAGACTGAGCTGAGTCGCTCCAGCCAAAGCTG	1503				
Db	8	GCCCCAGAGTAAACAGAA---GTGAGATAAAACTGAGTGAGTCGCTCCAGCCAAAGCT-	63				
Qy	1504	GATACCTCTATGTCAGTGAA---CGGTGACCAAGACTGAGTGTGGAATATTAGGGCCAAAG	1562				
Db	64	GATACCTCTATGTCAGTGAA---CGGTGACCAAGACTGAGTGTGGAATATTAGGGCCAAAG	123				
Qy	1563	ACTGCGCTAACCGGGAAAGTGTTGAGAGTGCTCTTGAGGAGTGCTCTCTTGAGGCAAG	1621				
Db	124	ACTGCGCTAACCGGGAAAGTGTTGAGAGTGCTCTTGAGGAGTGCTCTCTTGAGGCAAG	163				
Qy	1622	TGCCAGAAAACACACTTCTGTGTCACTGCCGCTGACCACACTGGAAAGCACATG	1681				
Db	184	TGCCAGAAAACACACTTCTGTGTCACTGCCGCTGACCACACTGGAAAGCACATG	243				
Qy	1682	ACAGCTTACTGTTCGACAGCAGGGCTTACTTCAGTGAGGGTTGCCTATAGCT	1741				
Db	244	ACAGCTTACTGTTCGATCAGCAGGGCTTACTTCAGTGAGGGTTGCCTATAGCT	303				
Qy	1742	ACACCCAGGTGGCTGGACTCTTGTGTTTATAGACAGGGCACATTGACTCTAG	1801				
Db	304	ACACCCAGGTGGCTGGACTCTTGTGTTTATAGACAGGGCACATTGACTCTAG	363				
Qy	1802	TGATGGAGCTGGAGGAGCTCTAGCAGGCTGGCTGAACTCCTGSC	1861				
Db	364	TGATGGAGCTGGAGGAGCTCTAGCAGGCTGGCTGAACTCCTGSC	423				
base count		122	a	138	c	127	g
origin				132	t		
Query Match		21.6%		Score 427.2; DB 12;		Length 519;	
Best Local Similarity		90.6%		Pred. No. 3.8e-78;			
Matches		489;	Conservative	0;	Mismatches		
Qy	1315	AGGACACAGCAGATCCGAGACAGACAGATGTCAGTAAGATAGGCTTGATGGCT	1374				
Db	519	AGGACACAGCAGATCCGTTGCAAGACAGATGTCAGTAAGATAGTGCATGGCT	460				
Qy	1375	GGAGGACGACAACAAATTATCCACGCTAGGGACACACCATATCCGCACAGGCCCTG	1434				
RESULT	28						
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	BASE COUNT	166 a	130 c	161 g	90 t
Db	459 GGGGAGACAAATCATTCCGCCATTGGACACGCCATTCCGCCAGGGCTGT	400			
Qy	1435 AACGCAAGGCCAGAGTAAACGAAGTGAGATAAAGACTGTGAGTCTGCCTCCAG	1494			
Db	399 AAGTCCAAGGCCAGAGTAAACGAAGTGAGATAAAGACTGTGAGTCTGCCTCCAG	340			
Qy	1495 CCCAGCGATCTTATGTCAGTAACGGTACAGTGAGTTGCAATT	1554			
Db	339 CCCAGCGACACCTCTATGTCAGTAACGGTACAGTGAGTTGCAATT	280			
Qy	1555 GGCGCAAGACCTGCTTAACGGAGTGTGTTGGAGAGCTGCTGCAACAGTCCAGTGAAT	1614			
Db	279 GGACCAAGAACCTGGCACCGGAAGTGTGTTGGAAATGGCCTCTGGAC	222			
Qy	1615 AGAGAGATGCCAGAAAACACACTTCCTGTTGACTCGGCCCTGACCAACAGTGGAG	1674			
Db	223 -----TTCCATGTTGACTGCGCCCTGACCAACAGTGGAG	187			
Qy	1675 CCACATGACAGTTACTGTCGATCAGCAGGGCTACTTCAGTCAGGGTTTCT	1734			
Db	186 CCACGTGACAGTTACTGTCGATCAGCAGGGCTACTTCAGTCAGGGTTTCT	127			
Qy	1735 TATAGCTACACCAAGGTGGCTGAGCTCTTGTGTTTATAGAACAGGGTACATGA	1794			
Db	126 TATAGCTACACCAAGGTGGCTGAGCTCTTGTGTTTATAGAACAGGGTACATGA	67			
Qy	1795 CTCTAAGTGTGATGGAGCTGAGGATCTATGCCAGGGACCTGCTTGAC	1854			
Db	66 CTTCAGTGGATGGAGACTGGCTGAGGACCTATGCCAGGTGGAC	8			
RESULT	29				
BE031265	BE031265	547 bp mRNA linear EST 09-JUL-2000			
LOCUS	129700 MARC 1PIG	Sus scrofa cdna 5', mRNA sequence.			
DEFINITION					
ACCESSION	BB031265				
VERSION	BB031265.1				
KEYWORDS	EST, pig.				
SOURCE					
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Getaertiodactyla; Suiha; Suidae; Sus.				
AUTHORS	Fahrenkrug,S.C., Fretking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grossie,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.				
TITLE	Design and use of two pooled tissue normalized cdna libraries for EST discovery in swine				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Smith TPL USAID, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390				
Email: smt@marc.usda.gov	Single pass sequencing. Bases called and alt_trimmed with phred and -minmatch 12 options.				
PCR PRIMERS	FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTCCAGTCACGAGC Plate: 65 row: H column: 4 Seq primer: ATTAGTAGTACACTTAAAG.				
FEATURES	source Location/Qualifiers				
source	1..547 /organism="Sus scrofa" /db_xref="taxon:9823" /clone_id="MARC_1PIG" /tissue_type="pooled" /lab_host="DIBI10B" (note "vector: pcMV SPORT6; Site_1: xbaI; Site_2: xbaI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos.")				
RESULT	30				
BB831869	BB831869	450 bp mRNA linear EST 19-NOV-2001			
LOCUS	BB831869				
DEFINITION	BB831869 RIKEN full-length enriched, mammary gland RCB-MC09 3', mRNA				
VERSION	JYg-MC(B)				
KEYWORDS	BB831869.1 GI:17101012				
SOURCE					
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Akimura,T., Arakawa,T., Caninici,P., Furuno,M., Henagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawaji,J., Koima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakizume,N., Saasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sobabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku,Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watanuki,A., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.				
TITLE	Riken Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)				

JOURNAL	Unpublished (2001)
COMMENT	Contact: Yoshihide Hayashizaki. Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
BASE COUNT	Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-reseq@riken.go.jp URL: http://genome.gsc.riken.go.jp/
FEATURES	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
source	wagi,K., Fujisawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
1	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
2	Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
3	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
4	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
5	e mouse tissues.
LOCATION/QUALIFIERS	Location/Qualifiers
1	1. location/qualifiers
2	/organism="Mus musculus"
3	/db_xref="taxon:10090"
4	/clone="G930019H09"
5	/clone_lib="RIKEN full-length enriched, mammary gland
6	RCB-0527 JYg-MC(B) cDNA"
7	/tissue-type="mammary gland"
8	/cell_line="RCB-0527 JYg-MC(B)"
9	105 a 102 c 114 g 129 t
BASE COUNT	ORIGIN
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7	/tissue-type="mammary gland"
8	/cell_line="RCB-0527 JYg-MC(B)"
9	105 a 102 c 114 g 129 t

JOURNAL	Unpublished (2001)
COMMENT	Contact: Yoshihide Hayashizaki. Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
BASE COUNT	Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-reseq@riken.go.jp URL: http://genome.gsc.riken.go.jp/
FEATURES	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
source	wagi,K., Fujisawa,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
1	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
2	Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
3	e mouse tissues.
4	Location/Qualifiers
5	1. location/qualifiers
6	/organism="Mus musculus"
7	/db_xref="taxon:10090"
8	/clone="G9300110B01"
9	/clone_lib="RIKEN full-length enriched, mammary gland
10	RCB-0527 JYg-MC(B) cDNA"
11	/tissue-type="mammary gland"
12	/cell_line="RCB-0527 JYg-MC(B)"
13	104 a 99 c 119 g 131 t
BASE COUNT	ORIGIN

Query Match 20.6%; Score 407.8; DB 9; Length 453;
 Best Local Similarity 97.8%; Pred. No. 4e-74;
 Matches 445; Conservative 0; Mismatches 7; Indels 3;
 Gaps 3;

Db 1 TGGATACCTTTATGTCAGTGACCGGAGCTTGTGATGTTGCAATTAGGGCCA 1561
 Db 1552 GACCTGGTAACGGARGTGTGAGGAAAGGCTCTGACCGACTCAGAGAGA 1621
 Db 60 GACCTGGTAACCGAAGCTGTTGGAGAAGGCTCTGACCGACTCAGAGAGA 118
 Qy 1622 TGCCCGAGAACACACTCTGTTACTGCCCTGACCAACACTGGAAAGCCATG 1681
 Db 119 TGCCAGAACACACTCTGTTACTGCCCTGACCAACACTGGAAAGCCATG 59
 Db 1682 ACCAGTAACTGTCGATCACAGGGGCTACTTCAGTTGAGGGTTGCTATAGCT 1741
 Qy 1742 ACCACCAAGTGCTGACTCTTGTGAGACAGCTGTTGGAGAATGGCTCTTGAC 1801
 Db 238 ACCACCAAGTGCTGACTCTTGTGAGACAGCTGTTGGAGAATGGCTCTTGAC 297
 Qy 1802 TGGATGGAGTGTGGAGATCTATGAGGCTGGAGCCCTGGCTTGAACTCTGCC 1861
 Db 298 TGGATGGAGTGTGGAGATCTATGAGGCTGGAGCCCTGGCTTGAACTCTGCC 357
 Qy 1862 TGCTCCAGCTTATGCTGAANTATGGGTTAGGTGGATAGGGAAAGGTGGAA 1921
 Db 358 TGCTCCAGCTTATGCTGAANTATGGGTTAGGTGGATAGGGAAAGGTGGAA 417
 Qy 1922 GTCAGTCGTTGAAATAAACGCATCTTC 1956
 Db 418 GTCAGTCGTTGAAATAAACGCATCTTC 452

RESULT 32

BB835693 BB835693 RIKEN full-length enriched, mRNA linear EST 19-NOV-2001
 DEFINITION BB835693 RIKEN full-length enriched, mammmary gland RCB-0527
 ACCESSION BB835693
 VERSION BB835693.1
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 412)

AUTHORS Akinuma,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kohima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakizume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,Y., Takaku,Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watanuki,A., Yasunishi,M., Yamamoto,M., and Hayashizaki,Y.

TITLE RIKEN Encyclopedia of Mouse Full-length cDNAs (Akinuma,T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
 1-7-2 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-6222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

Watanuki,M., Fujimaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Ichih,M., Carninci,P., Sugahara Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

e mouse tissues.

FEATURES

SOURCE

1. 412

/organism="Mus musculus"
 /ab_xref="taxon:10090"
 /clone="G30038609"
 /clone_1ib="RIKEN full-length cDNA RCB-0527 Jyg-Mc(B)"
 /tissue_type="mammary gland"
 /cell_line="RCB-0527 Jyg-Mc(B)"

BASE COUNT

96 a 91 c 111 g 114 t

ORIGIN

Query Match 20.6%; Score 406.2; DB 9; Length 412;
 Best Local Similarity 99.3%; Pred. No. 8.6e-74;
 Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 GCAATTAGTAGTGGCCAAACCTGGCTAACCGGAAGTGTGTTGGAAAGATGGCTCTTG 60

Qy 1546 GCAATTAGTAGTGGCCAAACCTGGCTAACCGGAAGTGTGTTGGAAAGATGGCTCTTG 1605

Db 61 ACCAGTCCAGAGATGCCAGAACACACTCTCTGTGTTACTGGCCCTGACAC 1665

Qy 1606 ACCAGTCCAGAGATGCCAGAACACACTCTCTGTGTTACTGGCCCTGACAC 1725

Db 61 ACCAGTCCAGAGATGCCAGAACACACTCTCTGTGTTACTGGCCCTGACAC 120

Qy 1666 ACTGGGAACCCACATGACCAAGCTGGCTAACCGAGTGTGCTACTCCAGG 180

Db 121 ACTGGGAACCCACATGACCAAGCTGGCTAACCGAGTGTGCTACTCCAGG 180

Qy 1725 GCTTTGCTATAGCTACACAGGTGTGCTGACTCCTTGTGTTATGACAGGG 1725

Db 181 GCTTTGCTATAGCTACACAGGTGTGCTGACTCCTTGTGTTATGACAGGG 240

Qy 1786 TCACATGGCTCTAAGTGGATGGAGCTGGCTGAGGATCTTGTGTTATGACAGGG 1845

Db 241 TCACATGGCTCTAAGTGGATGGAGCTGGCTGAGGATCTTGTGTTATGACAGGG 300

Qy 1846 CGCTTGAACCTCTCGCTGCTCCAGCTTATGCTGAAATTAGGGGAGGGTGTATA 1905

Db 301 CGCTTGAACCTCTCGCTGCTCCAGCTTATGCTGAAATTAGGGGAGGGTGTATA 360

Qy 1905 GGGAAAGCTGGGAACTTTCGCTGAAATAAAAGGAACTTTC 1956

Db 361 GGGAAAGCTGGGAACTTTCGCTGAAATAAAAGGAACTTTC 411

RESULT 33

BB77900 BB77900 RIKEN full-length enriched, mRNA linear EST 15-NOV-2001
 DEFINITION BB77900 RIKEN full-length enriched, Nullipotent stem cell CRL-2070
 ACCESSION BB77900
 VERSION BB77900.1
 KEYWORDS EST.

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	I (bases 1 to 423)
TITLE	Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
JOURNAL	RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.)
COMMENT	Unpublished (2001)
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)	Contact: Ioshihide Hayashizaki
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan	
Tel: 81-45-503-9216	
Fax: 81-45-503-9222	
Email: genome-ref@gsc.riken.go.jp/	
URI: http://genome.gsc.riken.go.jp/	
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
Hayashizaki,Y., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.	e mouse tissues.
FEATURES	source
source	/organism="Mus musculus" /db_xref="taxon:10090" /clone="G430042L20" /clone_lib="RIKEN full-length enriched, Nullipotent stem cell CRL-2070 NE cDNA" /cell_type="Nullipotent stem cell" /cellline="CRL-2070 NE"
BASE COUNT	100 a 93 c 111 g 119 t
ORIGIN	
Query Match	20.3%; Score 4014; DB 9; Length 423;
Best Local Similarity	98.3%; Pred. No. 8.4e-73;
Matches	416; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY	1534 AGAGTGTGTTGCAATTACTGGCCCAAGACCTTGCTAACCGGAGTGTGTTGGAGAT 1593
Db	1 AGACGATGTTGAATTAGTGGCCCAAGACCTTGCTAACCGAAGTGTGTT-GAAGT 59
QY	1594 GGCGCTCTGGACGAGCAAGAGAGATGCCAGAACACACTTCTGGTCACTGC 1653
Db	60 GACTCTCTGGACGAGCAAGAGAGATGCCAGAACACACTTCTGGTCACTGC 119
QY	1654 GCCCCGACACACTGGAGGCACATGACCACTTACGTTGATCAGCAGGGCTAC 1713
Db	120 GCCCCGACACACTGGAGGCACATGACCACTTACGTTGATCAGCAGGGCTAC 179
RESULT	34
LOCUS	AI428513/c
DEFINITION	403 bp mRNA linear EST 09-MAR-1999
MOLECULAR LENGTH	403 bp
MOLECULAR WEIGHT	mRNA
ACCESION	mo37h05.x1
VERSION	1
KEYWORDS	cdNA clone IMAGE:555801 3', mRNA sequence.
AUTHORS	AI428513
TITLE	AI428513.1 GI:4274439
JOURNAL	EST
COMMENT	house mouse.
FEATURES	source
source	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	I (bases 1 to 423)
TITLE	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stoeckoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Staller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watson,R. and Wilson,R.
JOURNAL	The WashU-NCI Mouse EST Project 1999
COMMENT	Unpublished (1999)
Laboratory/Qualifiers	Contact: Marra,M WashU-NCI Mouse EST Project 1999
FEATURES	source
source	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
BASE COUNT	4444
ORIGIN	
Query Match	20.2%; Score 3998; DB 9; Length 403;
Best Local Similarity	99.5%; Pred. No. 1.8e-72;
Matches	1.403
QY	1714 TTCCAGTTGCAGGTTTCGCTATAGCTACACCAAGGTGCTGGAGACTCCTTTGTT 1773
Db	180 TTCCAGTTGCAGGTTTCGCTATAGCTACACCAAGGTGCTGGAGACTCCTTTGTT 239
QY	1774 TATAGAACAGGTACATGACTPAAGTGGATGGAGTGGCTGAGGATCCTAAGCAGC 1833
Db	240 TATAGACAGCGTCACATGACTCTAAATGATGGAGTGGCTGAGGATCCTAAGCAGC 299
QY	1834 TGGAGCACCTGGCTGTGACTCCGCCCTCCAGCTTATGCTGAAATATGGGGT 1893
Db	300 TGGAGCACCTGGCTGTGACTCCGCCCTCCAGCTTATGCTGAAATATGGGGT 359
QY	1894 GAGGRGTTGATGGAAAGGTTGGGAAGTGTGTTCTGTAATAAAAGGATCTTC 1953
Db	360 GAGGTGTTGATGGAAAGGTTGGGAAGTGTGTTCTGTAATAAAAGGATCTTC 419

Email: genome-reseqc.riken.go.jp/
URL: <http://genome.gsc.riken.go.jp/>
Carninci,P., Shibata,Y., Hayashi,N., Sugahara,Y., Shibata,K., Itoh,
, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watabiki,M., Yoneda,Y., Ishikawa,T., Osawa,K., Tanaka,T., Matsuura
, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* .
10 (11), 1751-1771 (2000)
Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
, Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. *Genome Res.* . 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

FEATURES	Source
<p>1. . 393</p> <p>/organism="Mus musculus"</p> <p>/db_xref="taxon:10990"</p> <p>/clone="G33004/O220"</p> <p>/clone_id="RIKEN full-length enriched, mammary gland RCB-0527 JYg-MC (B) CDNA"</p> <p>/tissue_type="mammary gland"</p> <p>/cell_line="RCB-0527 JYg-MC (B)"</p>	<p>location/qualifiers</p>

Query Match	Best Local Similarity	Score	DB	Length
Matches 388;	99.0%	385.6;	DB 9;	Length 393;
Conservative	0;	Pred. No. 1.6e-69;	Mismatches 4;	Indels 0;
			Gaps 0,	
Oy	1565	CTGGCTAACCGGAAGGTTTGTGAATGTTGCCCTTGACAGTCAGTCAGAGAGATGC	1624	
Db	1	CTGGCTAACCGGAAGGTTTGTGAATGTTGCCCTTGACAGTCAGTCAGAGAGATGC	60	
Oy	1625	CCAGAAACACACTTCTGTGTCACTGGCCCTGACCCACACTGGGAGCCACATGACCC	1684	
Db	61	CCAGAAACACACTTCTGTGTCACTGGCCCTGACCCACACTGGGAGCCACATGACCC	120	
Oy	1685	AGTTACTGTTCGATCAGCAGGGCTTACCTTCAGTTCCAGGTTTGTCTTATAGCTACA	1744	
Db	121	AGTTACTGTTCGATCAGCAGGGCTTACCTTCAGTTCCAGGTTTGTCTTATAGCTACA	180	
Oy	1745	ACCAGGTGTGGTGGACTCTCTTGTATTAGAACAGGGCACATGACTTAAGTG	1804	
Db	181	ACCAGGTGTGGTGGACTCTCTTGTATTAGAACAGGGCACATGACTTAAGTG	240	
Oy	1805	ATGGGAGTGTGGAGGATCTATGCCGCTGGAGGACCCGCTGACTCTCTGCCCTG	1864	
Db	241	ATGGGAGTGTGGAGGATCTATGCCGCTGGAGGACCCGCTGACTCTCTGCCCTG	300	
Oy	1865	CTCCACCTTATGCTGCAATAATTATGGGTGAGGTGGTGTAGGAAGGTTGGGAAGT	1924	
Db	301	CTCCACCTTATGCTGCAATAATTATGGGTGAGGTGGTGTAGGAAGGTTGGGAAGT	360	
Oy	1925	TTCGTGTTAAATAAAGGGACTTTCTTC	1956	
Db	361	TTCGTGTTAAATAAAGGGACTTTCTTC	392	

Locus BI341090 **Definition** DEF368355 MARC 2PIG Sus scrofa cDNA 5' mRNA sequence.
Accession BI341090 **Version** EST
Length 571 bp **Organism** linear
Date 30-JUL-2001

VERSION BI341090.1 **GI:** 15034379
KEYWORD EST.
SOURCE pig.
ORGANISM *Sus scrofa*
REFERENCE 1 ({bases 1 to 571})
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS Fahrerug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grossel,W.M., Bennett,G.A., Lae Reid,W.W.

Query Match 18 6%; Score 367.6; DB 10; Length 769;
 Best Local Similarity 79.0%; Pred. No. 7.4e-66;
 Matches 463; Conservative 0; Mismatches 119; Indels 4; Gaps 2;

Qy 940 AACCTTGAGGCTGCCTC-GCGACCAATAGAACGGTCAACCGGCTGGTTTAGAGGCC 998
 Db 1 AACCTTGAACTGCACCACTGGCAGCTGAGACGTCGACGCCCTGGTTAGAGGCC 60

Qy 999 AGCCCTGAGGATGAGAACCGAGGCTTACACGCCACCCCTGGTATAGATGA 1058
 Db 61 AGCCCTGTGAA--GGTATGTCGAAGCTGCCGCGGCCATCCTCCGATATGA 117

Qy 1059 TCTCAATACACCTTGATGTAATACCCCTCACCCAGACCTTGCTCCCGCATG 1118
 Db 118 TCTCATGCTTACCTTGATGTAATACCCCTCACCCAGACCTTGCTCCCGCATG 177

Qy 1119 CCTCCCCAAGAACGCTGTGCTGGAGAGGGACGCCGCTCTCCATGAAATGTCCTCAAGAA 1178
 Db 178 TCTACTACGAAACATTGGCTAGAGAACGTCACACTCCCCAATCAGGATGTCCTCAAGAA 237

Qy 1179 GGTGACAAAGTCTCCAAGCCGGAGTCCCAGCTCTCACNGGTGGCCAGCTGAGTGAAGACTCTC 828

Db 238 GATATGCAAAAGCCCCCAGGAAGGATGCCAGCTCACTGGGTCGAGCTGTCAGG 297

Qy 1239 AGAGCTATGAGGAACTGCGCTGTGCTTCCTCTCATCGGAATGCTGTCTGG 1298
 Db 298 AGACCCAGATGAGAACCTGGTGTGCTTCCTATTTGTGTCGGAAATGCCATTCCTAGG 357

RESULT 38
 DEFINITION BFR38722 mRNA clone IMAGE:3864082 5',
 LOCUS BFR38722 linear EST 20-OCT-2000
 ACCESSION BFR38722
 VERSION BFR38722.1 GI:10745770
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Email: cgaps-r@mail.nih.gov
 REFERENCE 1 (bases 1 to 769)
 AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution by: The T.M.A.G.E. Consortium (LLNL)
 found through the T.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 URL: LLNL9605 row: a column: 11
 High quality sequence stop: 632.

FEATURES source
 1. .769 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="txxon:9606"
 /clone="IMAGE:3864082"
 /clone_1.lib="NIH_MGC_66"
 /tissue_type="adenocarcinoma"
 /lab_host="BHLB (phage resistant)"
 /note="Organ: ovary; Vector: pcMV-SPORT6; Site:1: NotI;
 Site: 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."
 BASE COUNT 184 a 212 c 217 g 156 t
 ORIGIN

Query Match 18 6%; Score 367.6; DB 10; Length 769;
 Best Local Similarity 79.0%; Pred. No. 7.4e-66;
 Matches 463; Conservative 0; Mismatches 119; Indels 4; Gaps 2;

Qy 1359 AGCCTTTGGCTTGGAGAGAACAAATTATCAGCCATTAGGGACACACATTAT 1418
 Db 418 AGGCTTCGAGGGCTCGGGGCCAGGTAGCTCTGTGAGCAAGTGTGAAGT 477

Qy 1419 CCGACCAGTGCCTTAAGTCCAGGGCAAGACTAAGCAGAATTCATCCGCTTAAGGAGGTGAAGGAGCAT 1478
 Db 478 CCGCCCATGCCCCCTTAAGCCAAAGCAAGTTAGGAGGTGAAGGAGCAT 537

RESULT 39
 DEFINITION AL529568 LTL_NFL01_NBC4 Homo sapiens mRNA clone CS0DD006YH09 5
 LOCUS AL529568 prime, mRNA sequence.
 ACCESSION AL529568
 VERSION AL529568.1 GI:12793061
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 932)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 COMMENT Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Séquençage
 BP 191 91006 EVRY cedex - France
 Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES source
 1. .932 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:6606"
 /clone="CS0DD006YH09"
 /clone_1.lib="LTL_NFL01_NBC4"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="BHLB"
 /note="Organ: brain; Vector: pcMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dt) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pcMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com>"
 BASE COUNT 226 a 242 g 200 t 11 others
 ORIGIN

Query Match 18 0%; Score 354.8; DB 9; Length 932;
 Best Local Similarity 75.9%; Pred. No. 3.2e-63;
 Matches 481; Conservative 7; Mismatches 140; Indels 6; Gaps 4;

Qy 769 GAACCTGGCTACAGGGTGAAGGATTGGTGTCTCTAGGACCAAGTGAAGACTCTC 828

		Seq primer: -40RP from Gibco High quality sequence stop: 382.
	FEATURES	Location/Qualifiers
Qy	source	1..585
Db	/organism="Mus musculus"	
Qy	/strain="FVB/N"	
Db	/db_xref="taxon:10900"	
399	/clone="IMAGE:3156502,"	
Qy	/clone_id="NCI-CGAP:Man6"	
949	/sex="female, virgin"	
Qy	/tissue_type="infiltrating ductal carcinoma"	
Db	/dev_stage="5 months"	
458	/lab_host="DH10B"	
Qy	/note="Organ: mammary; Vector: pCMV-SHORT6; Site_1: Sali"	
Qy	/Site_2: NotI; Cloned unidirectionally; Primer: Oligo dT.	
518	Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH	
Db		
Qy		
1068		
575		
TACCTTGAGTAATACCCCTCACCCAGACCTTGCTCCAGATGCCATGCCCTCAA 1127		
TACCTTGATGGTACTCCCCAGCGGCCCTCAGCATGGTACTACGA 634		
Qy		
1128		
GAACTGTGCTAGAGACTBACACTCCCATTAGGAGTCCTCCATGAGAATGCCAGAGGTGACACA 1187		
635		
AAACTTTGCTAGAGACTBACACTCCCATTAGGAGTCCTCCATGAGAATGCCAGAGGTGACACA 694		
Db		
Qy		
1188		
AGTCCTCCAAGCGGGAGTCCCAGCTCTCACTGGTGGCCACCGATGTAGAGAGCTAGA 1247		
695		
AGGCCCAAGGAGACTCCAGCYCTCACTGGTGGCCAGAGCTTTCAGGAAGCCAGA 754		
Qy		
1248		
TGAGGAGACTGCTGCTGCCCTCTCTCATCGGAATGCTGTCCTGGTCAAGAAC 1307		
755		
WGAGGAGCTGTTGGT-CYTCCCTATTGTTGTCGGAATGCCATCTAGCCAGAAC 813		
Db		
Qy		
1308		
GCCCCACAGACAGACAGAGAACATCCGAAGCAGCACAGTGTGTAAGATAGGTTGA 1367		
814		
GCCCCAGAGCCCAAGTCAGAGTCCTCTTGCAAGCAAGATGTTGTAAGGACAGGCTGA 873		
Qy		
1368		
TGGCTTGAGGAGCAGACAAATTGATCCAGCT 1401		
Db		
874		
TGGCTCGGCGGACAAATTCAACCRCCT 907		
RESULT 40		
AW910227		
LOCUS	AW910227	585 bp mRNA linear EST 25-MAY-2000
DEFINITION	ur79c12.y1	NCL-CGAP_Mam6 Mus musculus cDNA clone IMAGE:3156502 5'
		similar to TR_008854_008854 TRAF-INTERACTING PROTEIN ; mRNA sequence.
ACCESSION	AW910227	
VERSTON	AW910227.1	GI:8075467
KEYWORDS		
SOURCE		
ORGANISM	Mus musculus	
MUS musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 585)		
REFERENCE	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov	
Tissue Procurement:	Jeffrey Green M.D.	
CDNA Library Preparation:	Life Technologies, Inc.	
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNU)	
DNA Sequencing by:	Washington Genome Sequencing Center	
Clone distribution:	NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at: image.lnl.gov/image/html/resources.shtml	